## REMARKS

Claim 4 has been amended. Thus, claims 1-4 and 6-9 remain presented for examination. The amendment to claim 4 was made to place SEQ ID NO: 34 in order with the rest of the listed sequences so that it no longer appears by itself on a separate page. Thus, no new matter has been added. Reconsideration and withdrawal of the present objection and rejection in view of the amendments and comments presented herein are respectfully requested.

Claim objection

Claim 4 was objected to because the incorporation of "and" after "SEQ ID NO: 66" in the previous amendment pushed SEQ ID NO: 34 to the following page, such that it appeared out of sequence order in the claim. Claim 4 as amended removes SEQ ID NO: 34 from the following page, and places it in order with the other sequences.

In view of the claim amendment, Applicants respectfully request reconsideration and withdrawal of the claim objection.

Rejection Under 35 U.S.C. §102(b)

Claims 1-4 and 6-9 were rejected under 35 U.S.C. §102(b) as anticipated by Bruccoleri et al (*Nucl. Acids Res.* 26:4482-2286, 1998). The Examiner contends that Bruccoleri et al. teach all of the limitations of Claim 1 (generation of overlapping sequence alignments from pathogenic organisms; homolog matching; target sequence alignment for all sequences; alignment of just matching gene product against the corresponding gene product in the target; and exclusion criteria).

The present invention relates to a method of identifying conserved peptide sequences useful as drug targets by comparing genomes of various pathogenic organisms at the peptide level. This method comprises the following steps as recited in present claim 1:

> i) computationally generating overlapping peptide sequences from selected pathogenic organisms of length 'N',
>
> ii) computationally sorting the peptide sequences of length 'N' according to amino acid sequence,
>
> iii) computationally matching the sorted peptide sequences of length 'N' of the selected pathogenic organisms to produce matched common peptide sequences,

iv) computationally locating the matched common peptide sequences in their corresponding protein sequences to provide locations of said matched common peptide sequences and subsequently labeling the matched common peptide sequences with their origin and location;

v) computationally joining overlapping common peptide sequences to obtain extended conserved peptide sequences;

vi) comparing said extended conserved peptide sequences obtained in step (v) to host organism protein sequences to determine which of said conserved peptide sequences from said selected pathogenic organisms are not present in host proteins; and

vii) communicating said conserved peptide sequences from said selected pathogenic organisms not present in said host proteins to a user.

Thus, claim 1 relates to genome analysis at the peptide level. In contrast, Brucolleri et al. perform their analysis at the protein level, not by comparing peptide sequences across organisms to determine conserved peptide sequences that can be used as drug targets as recited in the present claims. Bruccoleri et al. state that "we have developed a simple and efficient computational tool which determines concordance of putative gene products that show sets of proteins conserved across one set of user specified genomes and not present in another set of user specified genomes." (see abstract) (emphasis added). Thus, Brucolleri et al. is concerned with determination of conserved proteins across genomes, not of conserved peptide sequences. In fact, Bruccoleri et al. state that "using this tool, we have successfully identified a number of promising protein targets for new antibiotic development conserved among several pathogenic bacteria." (emphasis added). Nowhere in Bruccoleri et al. is it taught to break down protein sequences into peptides and analyze the genome at the peptide level to determine conserved peptide sequences that can be used as potential drug targets. It is clear that the method disclosed by this reference only relates to genome analysis at the protein level. In fact, the word "peptide" is not mentioned even once in this reference. Thus, none of the steps recited in claim 1, all of which recite manipulations of peptide sequences, are disclosed by this reference. Thus, the claims cannot be anticipated.

In view of the comments presented above, Applicants respectfully request reconsideration and withdrawal of the rejections under 35 U.S.C. §102(b).

## CONCLUSION

Applicants have made an earnest effort to respond to all objections and rejections set forth in the Office Action, and submit that all claims are in condition for allowance. If any issues remain that could be resolved by telephone, the Examiner is cordially invited to contact the undersigned at the telephone number provided below. Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: 3/3/08

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